

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 3, 2002, 22:53:44 ; Search time 33.32 Seconds

(without alignments)
2110.117 Million cell updates/sec

-19

Title: US-09-497-822a-19
Perfect score: 4912

Sequence: 1 MEYQLGLGRVYBRPPSKTYR..... SVQVPKILSGRKPIYFHTQ 923

Scoring table: BL005M62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database : PIR68;*
1: Pirl1;*
2: Pirl2;*
3: Pirl3;*
4: Pirl4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	4.880	99.3	919	2	A39248	androgen receptor
2	4.788	97.7	910	2	A34721	androgen receptor
3	4.763	97.0	911	2	B34721	androgen receptor
4	4.265	85.6	902	2	B40494	androgen receptor
5	4.176	85.0	899	2	A35895	androgen receptor
6	1.676	34.1	344	2	I51330	androgen receptor
7	1.523	31.0	848	2	JG0194	androgen receptor
8	1.262.5	25.7	930	2	A25923	progesterone receptor
9	1.262	25.7	933	1	QRHUP	progesterone receptor
10	1.134	25.1	923	2	I53166	progesterone receptor
11	1.1218	24.8	786	2	A35466	progesterone receptor
12	1.1205	24.5	923	2	A39396	progesterone receptor
13	1.092	22.2	981	2	A41401	mineralocorticoid receptor
14	1.078.5	22.0	984	2	A29513	glucocorticoid receptor
15	1.065	21.7	795	1	QRRNG	glucocorticoid receptor
16	1.063.5	21.7	783	1	A25621	glucocorticoid receptor
17	1.054.5	21.5	776	1	S44047	glucocorticoid receptor
18	1.042	21.2	777	1	QRHUGA	glucocorticoid receptor
19	1.023	20.8	758	2	S60386	glucocorticoid receptor
20	1.003	20.4	771	2	A51273	glucocorticoid receptor
21	943.5	19.2	742	1	QRHUGB	glucocorticoid receptor
22	715	14.6	166	2	S35795	androgen receptor
23	502	10.2	595	2	I47140	estradiol receptor
24	491	10.0	586	1	ORXLE	estrogen receptor
25	48.5	9.9	600	1	QRRIIE	estrogen receptor
26	47.8	9.7	595	1	QRHUE	estrogen receptor
27	47.8	9.7	701	2	S60737	80K estrogen receptor
28	47.4	9.6	589	1	QRHHE	estrogen receptor
29	47.4	9.6	599	1	QRHSE	estrogen receptor

Score	Count
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219239	1
219238	1
219237	1

estrogen receptor
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estrogen receptor
estrogen receptor
FTZ-F1 protein - f
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gene COUP-TFI prot
transcription fact

ALIGNMENTS

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C;Accession: A39248; A30328; A40109; A60946; A27653; A40108; A40494; A32224; R;Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgs, H.N.; Migeon, C.J.; Wilson, E.M.; Proc. Natl. Acad. Sci. U.S.A., 86, 9534-9538 (1989) X	R;Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgs, H.N.; Migeon, C.J.; Wilson, E.M.; Proc. Natl. Acad. Sci. U.S.A., 86, 9534-9538 (1989) X
A;Title: Sequence of the intron/exon junctions of the coding region of the human andr	A;Title: Sequence of the N-terminal domain of the human androgen receptor is encoded by one, larg
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A;Title: Cloning of the human androgen receptor complementary DNA and localization to the	A;Title: Cloning of the human androgen receptor complementary DNA and localization to the
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R;Lubahn, D.B.; Joseph, D.S.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Ris-Sta	R;Lubahn, D.B.; Joseph, D.S.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Ris-Sta
Science, 240, 327-330 (1988) X	Science, 240, 327-330 (1988) X
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A;Title: Cloning of the human androgen receptor complementary DNA and localization to the	A;Title: Cloning of the human androgen receptor complementary DNA and localization to the
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Mol. Endocrinol., 2, 1265-1275 (1988) X	Mol. Endocrinol., 2, 1265-1275 (1988) X
A;Title: The human androgen receptor complementary deoxyribonucleic acid cloning, se	A;Title: The human androgen receptor complementary deoxyribonucleic acid cloning, se
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A;Cross-references: GB:M20132; PID:9178627; R;Trapani, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Willard, H.F.; French, F.S.; Ris-Sta	A;Cross-references: GB:M20132; PID:9178627; R;Trapani, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Willard, H.F.; French, F.S.; Ris-Sta
Biochem. Biophys. Res. Commun., 153, 241-248 (1988) X	Biochem. Biophys. Res. Commun., 153, 241-248 (1988) X
A;Title: Cloning, structure and expression of a cDNA encoding the human androgen rece	A;Title: Cloning, structure and expression of a cDNA encoding the human androgen rece
A;Reference number: A27653; MUID:88240407	A;Reference number: A27653; MUID:88240407
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F: 550-570/Region: zinc finger
F: 586-610/Region: zinc finger

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Qy	361	YQSDYYNNPLLAGPQQPPPHARLKLNPFLDYGSAWAAAACQRYGDLASLHGAG	420						
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Qy	421	AAGPGSGPSAANSSWWHTLTABEGQLYPCGGGGGGGGGGGGGGGGGGGGGGGG	480						
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Qy	481	VAPGYTRPPOGLAQESEDTAPDWYPGGMYSRVPYSPPTCVKSENGPWWDSGSPYGD	540						
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Qy	601	SRNDCTIDKERRKNCPSCRRLRKYCEAMTGLGARKLKLNLKQEGEEASSTTSPEET	660						
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Qy	661	QKTVSHIEGYEQCPIFLVLEAIPEGVCAHDNNOPDSFAALLSSLNELEGEROLHVY	720						
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Qy	721	KWAALKPCFRNLHVDDOMAIVOSWNGLMVAMGWSFTNNSRMLYFAPDLYENYRMH	780						
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Qy	781	KSRMYSQCVRMRHLSOFGWLIOTPQFLCKKALLLFSITIPVDGLKNO-KFDFDELRMNYI	839						
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B40494	androgen receptor - rat	Rattus norvegicus (Norway rat)		Qy	343	LPSTLSLYKSGLADEAAAYOSRDYNNPLLAGPPPPPPIPHARIKLENPLDYGSAWA	402
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C;Accession: B40494; A36283; B40108	R;Chang, C.; Kokontis, J.; Liao, S.	Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988		Qy	403	AAACRYCGLDLASHGAGAGPGGSPPSAAASSWHTLFTAAFEQGOLYGPCCGGGGGG	462
R;Tan, J.; Joseph, D.R.; Lubahn, D.B.; Sar, M.; French, F.S.; Wilson, E.M.	A;Title: Structural analysis of complementary DNA and amino acid sequences of human and mouse androgen receptor: primary structure, autoregulation of its messenger RNA; Reference number: A40494; MUID:89017168	A;Accession: B40494		Db	397	AAAACRYCGLDLASHHGGSGAVPSGSPPATASSWHTLFTAAFEQGOLYGP-	445
Mol. Endocrinol. 2, 1276-1285, 1988	A;Status: preliminary	A;Molecule type: mRNA		Qy	463	GGGGGGGGGGGGAGAVALPYGTRPQQLASQESDTPADWYPPGMVSRVPPYSPPTC	522
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R;Yarborough, W.G.; Quarls, V.E.; Lubahn, D.B.; Sar, M.; French, F.S.; Wilson, E.M.	A;Cross-references: GB:M20133; PID:g9202895	A;Cross-references: GB:M20133; PID:g9202895		Qy	523	VKSENGPWWMSGYGDNMLRATTADHVLPIDYFPPOKTCILCDEASGHYGAUTCGS	582
J. Biol. Chem. 265, 8893-8900, 1990	A;Residues: 1-388; S'	A;Residues: 1-388; S'		Db	502	VKSENGPWWMSGYGDNMLRATTADHVLPIDYFPPOKTCILCDEASGHYGAUTCGS	561
A;Title: A single base mutation in the androgen receptor gene causes androgen insensitivity syndrome; Reference number: A36283; MUID:890112209	A;Accession: A34943	A;Molecule type: mRNA		Qy	583	CKVFVRAAKGOKYLCASRNDCTIDKFRKNCPSCRUURKYEAGMTLJARKLKLGNLK	642
A;Cross-references: GB:M265; Simental, J.A.; Joseph, D.R.; Sar, M.; Lubahn, D.B.; Wilson, E.M.	A;Cross-references: GB:M265; Simental, J.A.; Joseph, D.R.; Sar, M.; Lubahn, D.B.; Wilson, E.M.	A;Cross-references: GB:M265; Simental, J.A.; Joseph, D.R.; Sar, M.; Lubahn, D.B.; Wilson, E.M.		Db	562	CKVFVRAAGSKQKLCASENDCTIDKFRKNCPSCRUURKYEAGMTLJARKLKLGNLK	621
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Science 240, 324-326, 1988	A;Accession: A36283; MUID:890112209	A;Cross-references: GB:J05454		Qy	703	ALLSSLNEGLERQLYHVKVAKALPGRNQPSDFA	681
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Science 240, 324-326, 1988	A;Accession: B40108	A;Molecule type: mRNA		Qy	823	DGLKNKFEDELRMRNYKELDRITACKRKNPNTCSRRYFOLKLDSVOTARELHQFTF	882
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A;Residues: 1-265, 8893-8900, 1990	A;Status: preliminary	A;Molecule type: mRNA		Qy	883	DLLIKSHMVSVDPEPMMAITISVQVKPILSKGVKPYFHFO	923
A;Title: Unassigned erba-related proteins; erba transforming protein homology	A;Accession: B40108	A;Cross-references: GB:J05454		Db	862	DLLIKSHMVSVDPEPMMAITISVQVKPILSKGVKPYFHFO	902
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C;Superfamily: unassigned erba-related proteins; erba transforming protein homology	A;Accession: B40108	A;Accession: B40108		Biochim. Biophys. Res. Commun. 171, 697-704, 1990			
A;Keywords: DNA binding; zinc finger	A;Accession: B40108	A;Accession: B40108		A;Title: Molecular cloning of androgen receptors from divergent species with a polypeptide cDNA probes from dog, quinea pig and clawed frog.			
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A;Keywords: DNA binding; zinc finger	A;Accession: B40108	A;Accession: B40108		Mol. Endocrinol. 4, 1600-1610, 1990			
F;578-602/Region: zinc finger	A;Accession: B40108	A;Accession: B40108		A;Title: Structure and size distribution of the androgen receptor mRNA in wild-type and homozygous transgenic mice			
A;Status: preliminary	A;Accession: B40108	A;Accession: B40108		A;Reference number: A37255; MUID:9113343			
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F;578-602/Region: zinc finger	A;Accession: B40108	A;Accession: B40108		R;Charest, N.J.; Zhou, Z.; Lubahn, D.B.; Olsen, K.L.; Wilson, E.M.; French, F.S.			
A;Status: preliminary	A;Accession: B40108	A;Accession: B40108		Mol. Endocrinol. 5, 573-581, 1991			
A;Residues: 540-611 <CH2>	A;Accession: B40108	A;Accession: B40108		A;Title: A frameshift mutation destabilizes androgen receptor messenger RNA in the Tf			
C;Superfamily: unassigned erba-related proteins; erba transforming protein homology	A;Accession: B40108	A;Accession: B40108		A;Reference number: A37908; MUID:92017874			

RESULT
RHUP
Progestester
; Alterna
; Contain
; Species
; Date: 3
; Accessi
; Kastner
; MMBQ J. 9
; Title:
; Referen
; Accessi
; Molecul

Query	Match	Score	DB	Length
Query Match	25.1%	Score 1234;	DB 2;	Length 923;
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Qy	15 PSKTYRGA-----FQNLFOSVREVNQNPGRPEASAAPP---GASLLLQQQQ	61		
Db	19 PSPTHVGSPILLARDPDPQ-----GSQHSDASSVSVSIPITSLDRLFSRSC	65		
Qy	62 QQQQQQQQQQQQQQ-----QQQQQETS PROQQQQGEGDSPAHRRGPTGYL	110		
Db	66 QAQELPDEKTNQNOQLSDVEGAFSGYEASRRSRNPRAPERDSRLLDs-----	113		
Qy	111 VLDQQQSPQSALECHPBRGC-----VPEPGAAVASKGFLQQLPAPPDE-	157		
Db	114 VLDLTLAPSGEPOSQTSP-----ACEAITSRQLCFGPPELPDRSPVATKGLLSPLMSRPESK	171		
Qy	158 DDSA-----PSTLS---LIGPTF-----PGLSSCSADLKD---ILSEA	190		
Db	172 AGDSSCTGAGOKVLPKAVSPRQLLPTSSAHWPGAGVPSQOQPAVEEDGGIETEG	231		
Qy	191 STMOLLIQQQQEAVSEGSSGRAREASGAPTSKONYLGTTSTI-SDNAKEBLCKAVSVM	249		
Db	232 SAGPLIKSKPRALEGMCSSGGVTANAPGAAP-----GVITLVPKEDRSSESAPRVSLQ	284		
Qy	250 GLGV-----EAELHLSPOEQLRDCM-----YALGV	277		
Db	285 DAPVAPGRSPRPLATTVVDFHYPILPLNHALLAARTPQLLSGDSDYGGAAQVPFAPPGRS	344		
Qy	278 PPAVR PTCPACPLAECKSLLDDSAKGSTED-TAEYSPTFKGGTYKGLGELESLGCGCSAA	335		
Db	345 PSAPSPPVPCGDFPDC----TYPPECDPKEDGFPYGEFQPGLKLKEE-----EATEAA	396		
Qy	336 GSSGTBLPLSTSLSYLKSGALDEAAAYOSRDIYNNFPLLAGPFFFFP-----PPPHPHARIKLEN	393		
Db	397 SRS-----PRPYL-----AGASAATTPDGPL-----PPRPRPAPPSRP-----4.30			
Qy	394 PLDYGSAWAAAAOCRYGLDLS-----DGAGAAGPGGSS-----PSAAAGSSWH	438		
Db	431 ---GEA-AVARPSAAVSPVSSSGSALECLYKAEGAAPTGQSFAFLPKCPKAASS---	481		
Qy	439 TLFTAERGQLYGPCCCCGGGGGGGGGGGGGGGEAVAPYGTYRPPQGLAGQES	498		
Db	482 -CLPRUSLPAAP-----TSSAAPAY-----TPLLGLNS-----509			
Qy	499 DFTADPVWYPGGMV-SRVPPYSPPTCYVKSEMGFWMD-----SYSPGYDMRLETARDH	549		
Db	510 --LPQYQQAVALKDPSQVQY-----PYLNLYLRPDSBASQSPQYQFDSDL-----552			
Qy	550 VLIDYYFPQRTCLIGCDEASGCHGCAUTCGSSCKYFKAEGKQKYLACASRNDCDTIK	609		
Db	553 -----PQKCLIGCDEASGCHGCVKFEFRAMEQHNLYLCAQRNDCLVDK	603		
Qy	610 FRRKNCPSCLRKCYEGMTLGARKLKKLGNLKLQE--EGEA--SSTSSTPBTETT--OKL	663		
Db	604 TFSPNQETQVLQPLNLMISIEPDVYAHGHDNTKPDTSILTSINQLGERQSLSSVWK	663		
Qy	664 TVSHIEGECOP-----PQVNLAEIPEGVVAHQNQDPSFAALLSSNELGJEROLVHVVKWA	723		
Db	724 KSLPGERNRNHIDQDTLQYSWMSLAMYFGLGWRSYKHSQMLYFAPPDLINNEORMKELS	783		
Qy	784 MYSQCVRMHLSQFFGWLQITPQFPLCMKALLFLSTIPDVGKKNKFDELRMYIKEEL	843		
Db	784 FYSUCLTMWQIPOEFVKLCYTHEFCLVKMVLINTPLGQSLQSSPMEMRSYIREI	843		
Qy	844 RITACKRNPSCSRPNTCLKLDSVOIARELHOFTDPLLIKSHMVSDPEMMAEII	903		
Db	844 KAIGLROKGVPVSSORFYQLKLDSLSDVQKHLCYLNTFOSRALAEEPFMMSMVEI	903		

QY 904 SVQYPKILSGKKVKPIYFH 921
 Db 904 AAOQPKTLAGMVKLLEH 921

RESULT 11

A35466 Progesterone receptor form B - chicken

N; Contains: progesterone receptor form A

C; Species: Gallus gallus (chicken)

C; Cross-references: GB: M32732; PIDN: AAA49011.1; PID: g212553

R; Conneely, O.M.; Dobson, A.D.W.; Tsai, M.J.; Beattie, W.G.; Toft, D.O.; Huckaby, C.S.;

Mol. Endocrinol. 1, 517-525, 1987

A; Title: Sequence and expression of a functional chicken progesterone receptor.

A; Reference number: A40903; MUID: 88166640

A; Accession: S06284; Molecule type: DNA

A; Residues: 1-786 <JEL>

A; Cross-references: EMBL: Y00092; PIDN: CAA66282.1; PID: g63745

R; Conneely, O.M.; Dobson, A.D.W.; Tsai, M.J.; Beattie, W.G.; Toft, D.O.; Huckaby, C.S.;

Mol. Endocrinol. 1, 517-525, 1987

A; Title: Sequence and expression of a functional chicken progesterone receptor.

A; Reference number: A40903; MUID: 91042592

A; Status: Preliminary

A; Molecule type: mRNA

A; Residues: 1-64, 'E', 65-786 <CON>

R; Conneely, O.M.; Sullivan, W.P.; Toft, D.O.; Birnbaumer, M.; Cook, R.G.; Maxwell, B.L.;

Science 233, 767-770, 1986

A; Title: Molecular cloning of the chicken progesterone receptor.

A; Accession: A24661; MUID: 86289413

A; Molecule type: mRNA

A; Residues: 128-133, 'E', 135-147, 'E', 149-164 <CO2>

A; Note: the authors translated the codon CAG for residue 7 as Glu and CAG for residue 21

R; Jeltsch, J.M.; Krozowski, Z.; Quirin-Stricker, C.; Gronemeyer, H.; Simpson, R.J.; Garr

Proc. Natl. Acad. Sci. U.S.A. 83, 5424-5428, 1986

A; Title: Cloning of the chicken progesterone receptor.

A; Reference number: A24312; MUID: 862287271

A; Accession: A24312

A; Molecule type: mRNA

A; Residues: 417-490 <JE2>

A; Cross-references: GB: M14280; PIDN: g212607; PIDN: AAA49039.1; PID: g212608

R; Birnbaumer, M.; Hinrichs-Rosello, M.V.; Cook, R.G.; Schrader, W.T.; O'Malley, B.W.

Mol. Endocrinol. 1, 249-259, 1987

A; Title: Chemical and antigenic properties of pure 108,000 molecular weight chick proges

A; Reference number: A40911; MUID: 88288199

A; Status: Preliminary

A; Molecule type: protein

A; Residues: 128-133, 'E', 135-147, 'E', 149-164-546-558 <BI>

R; Simpson, R.J.; Grego, B.; Govindan, M.V.; Gronemeyer, H.

Mol. Cell. Endocrinol. 52, 177-184, 1987

A; Title: Peptide sequencing of the chick ovulet progesterone receptor form B.

A; Accession: A40911

A; Molecule type: protein

A; Residues: 136-153, 168-174, 195-228, 526-537, 'X', 539, 546-563 <SM>

C; Genetics: A; Introns: 4 00/2; 451/1; 490/1; 591/1; 639/2; 683/1; 735/3

C; Superfamily: Progesterone receptor; erba transforming protein homology

C; Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
 F; 1-766/Product: progesterone receptor form B #status predicted <MA>
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 F; 421-441/Region: zinc finger
 F; 457-481/Region: zinc finger

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 Best Local Similarity 33.4%; Pred. No. 3.7e-57;
 Matches 325; Conservative 128; Mismatches 259; Indels 260; Gaps 30;

QY 13 RPPSKTYGAFQNLQFSYREVIONPGPR-HPEAASAAPPAGASLLLQQQQQQQQQQQQ 71
 Db 10 RAPSSARDGV-----LLQAPPSSREAEIGDVALDG--LLYPRSSDDEEEEEEENE 57

QY 72 QQQQQQQQQQETS PROQQQQQGEDGSPQAHRGPTGYLVLDFFQPSSQALECHPER 131
 Db 58 EEEEEEEDRDQPSYR-----EEEEEEDRDQPSYR----- 85

QY 132 GCVEPGAAVAAASKGLPQLPAPDEDASAP-----LSSLGPTPECLSSCSADLKDL 187
 Db 86 -----PGGSSL SKCILDSW-----DTFLAPAAHAAPWSLGPPEPV----- 121

QY 188 SEASTMQLLQQQQQEASEG-SSSGGRAREASGAPTSKSDNYLGGTSTISDNAKELCKAVS 246
 Db 122 -EVVVPAPMSPRGPEKQAVDAGPAGPSPRPGP-----LWPGDSLNVAK 167

QY 247 VSMGLGVEELEHLSPGEQLRGDMYAPLGVPPAVRPTCPALAECKGSLDDSAKGKSTE 306
 Db 168 ARPG-PEDSENAP-----LPGAAERGEFPERDA----- 196

QY 307 DTAFYSPFKGGTITKGLBESLGSAGASSSTLEDPSTSLSYKASLDEAAYOSRDY 366
 Db 197 -----GPCEGGL-----APAAAASPAAVE-----FGA-----GQDY 222

QY 367 YNFPLALAGPQQPPPHHARIKLENPLDYGSAWAAAACOGRYGDIALSHGAGAAGPGS 426
 Db 223 LHPPI-----LPLNSAFLASRTR-QLJOVEAYTDGSAGPPRS 258

QY 427 GPSAAASSSWHITLEAAEGOLYGPCCGGGGGGGG-----GGGGGGGGGGG 475
 Db 259 -SPSVPAAD-----LAEYG-YPPPDKEGPFAYGFQFOSALKIKEEGVGLPAAAPPFLG 309

QY 476 GEAGAVAPYGYTRPQQGLAQPSDFTA-----PDWVPPGAVSRVPPYS----- 519
 Db 310 AKA-----APADFAQPPR-AQOPSPSLEYVLAKEPPLPGAVPPQKPLSTSAAPPGL 364

QY 520 -----PTCVKSEMGPWMWDYSSGPY-GDMRLBTARDIVLPIDYYFPQKTC 563
 Db 365 YSPGLNGHQAQLGEPAAVYKEQLPL-----CPPYLSGVVRPDTETQSQQSFESDFQKTC 421

QY 564 LIGCDEASGHCIYGAUTCGSKVFFKRAEGKQYLCASTRNDCTIKFRRNCPSCRLRKC 623
 Db 422 LIGCDEASGHCIYGAUTCGSKVFFKRAEGKQYLCASTRNDCTIKFRRNCPSCRLRKC 481

QY 624 YBAGMTLGAARKLKGKLNK-----LOEEGEASSSTSPTETKTQVTVSHIE 669
 Db 482 CGAGMVIGGRKEFKLNMKVTRLTDYALQOPAVLODE-----TOSTORLUSFSPNQ 532

QY 670 GYECPQIFLVNLEAIEPGVYCAHGDNNOPOPSFAALLSLNEGLERQVHVVKWAKALPFC 729
 Db 533 EIPFVPMSVLRGEPEVYVAGYNTKPTPSSLTSHLCLPQLCILQVKNKLGE 592

QY 730 RNLHVDQMAVYIQSYWMGLAVFAMGWSRSTINVSMLYFAPDLYNEYRMHKSRMSYSCV 789
 Db 593 RNLHIDQTTLIQQSYWSMSLAVFANGWRSYKHSQMLYFAPDPLLINEORMKESFSCLL 652

QY 790 RMRHLSQEFQWLMQIPTQFELCMKALLFSTIPIVQDGKLNKFQFDELARMYTKELDRILLACK 849
 Db 653 SMWQLDQEFTYRLQVSQEFFCMKAUILLNIPLEGLRSQOFDMRTSYIRELVKAIGLR 712

QY 850 RKNPTSCSRRFYQLTKLDSVQPIAREHQFTEDLIKSHMVSDFPEMMAEIIISVQVPK 909

Qy	125	-----LECHPERGCVPEP--GAAVAASKGL-----	-PQQLPAPPDEDDSAA 162	Science 237, 268-275, 1987
Db	179	AIVKSPUICHEKSSSSVSPGNSMSSSTTSGFSPVWHSPTTQGTSLTCs	238	A;Title: Cloning of human mineralocorticoid receptor complementary DNA: structural an
Qy	163	PST-----	LSLGBTFPGLSSCSADIKRDILSEASTMQLQQ 198	A;Reference number: A29513 ; MUID:87263386
Db	239	PSVENRGSRSHSPTHASNNGVSPPLSSMKSPISSPPSHSS- -VRSpvSPNNVPLRSS	296	A;Accession: A29513
Qy	199	QQREA-----VSEGSSGRAEASGAPS SKDNYLGCTSTISDRAKCKAVSVNG	250	A;Molecule type: mRNA
Db	297	VSSPANLNNSRCSYSSPNNNTNRLSSPASTVGIG- -SPISNAFSYATSGASAGAG	354	A;Residues: 1-984 <ARR>
Qy	251	LGVIALEHLSPG---EQLRGDCMYAFLGYPAPAVRTPCZPL- ---AECKGSLLDD 299	F:601-680/Domain: erbA transforming protein homology	
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Qy	300	SAGKSTEDTAEYSPFKGGTYKLEGESLGCGSAANGSSCTELFSTLSYKSGALDEA 359	F:639-663/Region: zinc finger	
Db	411	CLGGNSK-ISPSSPFSPVBIQK-ESSRKHSCSGASFKNPNTVNPFFMDSYF- 464	Query Match Score 1078.5; Pred. No. 1.1e 49;	
Qy	360	AYQRDYYNFPPLAGAPP-----PPPPIPHARIKENLPDYGSAWAAAACQRYGDL 413	Best Local Similarity 32.8%; Gaps 30;	
Db	465	---KDYSLS-GILGPVPFGDFGSCDSAFP- -VGIKOPBDOS-----YYPE 506	Matches 300; Conservative 101; Mismatches 254; Indels 259;	
Qy	414	ASLHGAGAGGGPSGSPSAAAASSWHTLFTAEQOLYGPCCGGGGGGGGGGGG 473	Query 98 SPOQAHRRGPTGYL-----VIDEEQQP-SQPOSALECHERGCVPEP ---GAAYAASK 145	
Db	507	ASIPSSAIVGNSG----GOSFY-----	Db 238 SPNAENRGRSRSHSPAHASVNGSPLSPLSSMKSSTSSPSPHCSVKSPrSPNVTRSSV 297	
Qy	474	GGGAGAVAPGYTRPQGLAGAQESDFTAPDWWPGGMYSRVPSPSPCIVKSEMPWMS 533	Qy 146 GLPQQL-----PAPPDED-----SAPFSTL SLLQP-----TFPGJLUSCSADLK 185	
Db	527	---RIGQGTISLRSRSPRQSFQH-----LSSFP-PVNTLIVES---WR-- 562	Db 298 SSPANINNSRC-SVSSPSPSNNNRSTLSSSPASTVGSCISPVNNAFSFTYASGTSAGSSSTLRD 357	
Qy	534	YSGPYGDMRLIETARDHVLPIDYFP-----	Qy 186 ILSEASTMQLQQQ ---OQEAVSEGSSSGRA -----REASGAPTSSKDNVYGGT 231	
Db	563	---PRGD---LSRRSDGYPVEYIENVSSSTTURSVTGSRSKICLVGDEASGHYG 617	Db 358 VVPSPDTDQEKGAEVYPPPTTVEVSATISGVITQQLNIVQYTRPEPDQAFSSS ---CLGGN 414	
Qy	577	ALTGCSKCKVFRAAGKGOKYWLCASENRTDTPKFRKNCPSCLRKYEAGMTLGARKLK 636	Qy 232 STISDNNAKELCKAVSVMSMGVLEAHLSPEGLRGDOMYAPLLGCVPPAVRPTPCAPLAE 291	
Db	618	YVTCGSKCKVFRAVEQGHNYTLCAGRNDCTIDKIRRNCPACRQCLQAGANLGARKSK 677	Db 415 SKINSDS-----SFSVIJKQESTKHSCTSGTSEFKGN-----PTVNPFP ----- 451	
Qy	637	KIGNLK-LQEE-----GEASSTTSPTEETT-----QKLTVSHTEGYECQP 675	Qy 292 CKGSELDDASAGKSTDETYAY- -SPEFKGGYTGLEGESLGCSSESSAAGSSGTLLEPLSTSL 349	
Db	678	KLGKLGLHEQPQQPQQPPQQPSBEGTYIAPKEPSVNSALVPQLTSITH---ALTP 733	Db 452 ---FMDGSEFSMDKDYSLSSCILGPVPGFDG---NCEES----- 487	
Qy	676	TFLNLAIEAIEGVVCAAGHDNQNPDSFAALLSNELGRLHYVKWAKALDFRNHLHD 735	Qy 350 YKSGALDEAAAYQSRYDYYNPLALAGPPPPPPhiARIKLENPIDYGSWAAAAAQCR 409	
Db	734	SPAMILNIEETVYAGDNSKPDASLSTUNRLAAKQMTQVVKAKVLFGRNLHVD	Db 488 -----GFPVQCIKQF----- 501	
Qy	736	DOMAVIQYSWMLMFAMGWSRFVNNSRMLYFADPLVNEYKMHKSRYMSCVNRHLS 795	Qy 410 YGDLASLHAGAACPGGSSPSAASSAAASLNLFTAERGQLYGPCCGGGGGGGGGGGG 469	
Db	794	QFVRLQLTPEYYSIMKVLNLSTVKOGLSQAAFEEMRTNTIKEURKAVT-- KCPNS 910	Db 502 YYPEASIPSAIVGVNSG-----GQSFHY----- 525	
Qy	796	QEFQWQIQTPEFLCKMALLFSTIPDGLKNOKFDELRYNIKEIDLRIACKRKNPTS 855	Qy 470 GGGGGGEAVAVAPGYTRPQPLAGOQESDFTADPWYPGGMVSRVYPSPCTVKSEMP 529	
Db	854	IQFVRLQLTPEYYSIMKVLNLSTVKOGLSQAAFEEMRTNTIKEURKAVT-- KCPNS 910	Db 526 -----RIGAQQTISLRSRSPFQH-----LSSPP- PNTLVBs----- 559	
Qy	856	CS---RREVQTKLDSLQVPIARELHQFLDLSVDFPEKMAEFTVQVKPLS 912	Qy 530 WMDSYSGPQDMRLETAEDHVLPIDYFP-----PQK2CLICDEA8G 572	
Db	911	SGSNQWRFQYQTLKLDMSLDSLLECFYTFRESQALKVFPAMLVETTDQLEPKVES	Db 560 WKS -----HGD- -LSSRSDGTPVLEYIPENVSSSTLRSYSTGSSRSPSKCLVCGDSEA 612	
Qy	913	GKVKPTYFH 921	Qy 533 RKLKKLGNLK -LQEGRASS-----TTSPTTEET-----OKLTVSH 667	
Db	971	GNAKPLYFH 979	Db 673 RKEKKGKLNK-----TTSPTTEET-----OKLTVSH 667	
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N;Alternative names: aldosterone receptor - human				
C;Species: Homo sapiens (man)				
C;Accession: A29513				
R;Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, T.M.; Handelin, B.L.; Housman, D.E.				
G;Date: 31-Mar-1990 # sequence_revision 31-Mar-1990 # text_change 20-Sep-1999				
Qy	728	GPNLHVDQMAVIOYSWMLMFAMGWSRFVNNSRMLYFADPLVNEYKMHKSRYMSQ 787		
Db	789	GFKNPLIEDQTLIOYSWMLCSSLFALSWSRYSKHTNSQFLYFADPLVNEEKHQMSANYEL 848		

Qy	788	CVRMRHLSOEGWLIQTPEFLCMKALLFSLIPVDGLKNQKFDELRLRNYIKELDRITA	847
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Db	849	CQGMHQISQFVRLQLTPEEYIMKVLLSTPKDGKSQAFFEMRTNTKELKRMVT	908
Qy	848	CKRNPTTSRSRQYQTLKSDSQTAPTELQFTDLIKMSVSDPPEMAEISVQ	907
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Db	909	KCPNNSGQWQRFYQTLKLDMSHDLVSDLERFCYTFRESHALKVEFPAMLVETSQL	968
Qy	908	PKLSGKVKRPIYFH	921
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Db	969	PKVESGNAPRPLYFH	982
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C;Species: Rattus norvegicus (Norway rat)			
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 22-Jun-1999			
C;Accession: A24194; S02475; A27294; S33891			
R;Miesfeld, R.; Rusconi, S.; Godowski, P.J.; Maller, B.A.; Wikstrom, A.C.; Gusell, Cell 46, 389-399, 1986			
A;Title: Genetic complementation of a glucocorticoid receptor deficiency by expression of			
A;Reference number: A24194; MUID:86272086			
A;Accession: A24194			
A;Molecule type: mRNA			
A;Residues: 1-95 <MIE>			
A;Cross-references: GB:MI4053; NID:9204271; PIDN:AAA41203.1; PID:g204272			
R;Severe, Y.; Wieland, S.; Schaffner, W.; Rusconi, S.			
EMBO J. 7, 2503-2508, 1988			
A;Title: Metal binding 'finger' structures in the glucocorticoid receptor defined by site			
A;Reference number: S02475; MUID:89052664			
A;Status: not compared with conceptual translation			
A;Molecule type: mRNA			
A;Residues: 40-539 <SEV>			
R;Chang, C.-J.; Kokantis, J.; Chang, C.T.; Liao, S.			
Nucleic Acids Res. 15, 9603, 1987			
A;Title: Cloning and sequence analysis of the rat ventral prostate glucocorticoid receptor			
A;Reference number: A27294; MUID:88067783			
A;Accession: A27294			
A;Molecule type: mRNA			
A;Residues: 1-97,'D',99-225,'G',227-259,'D',261-344,'T',346-515 <CHA>			
A;Cross-references: GB:Y00489; NID:56324; PIDN:CAA68545.1; PID:956325			
R;Gearing, K.L.; Gustafsson, J.A.; Okret, S.			
Nucleic Acids Res. 21, 2014, 1993			
A;Title: Heterogeneity in the polyglutamine tract of the glucocorticoid receptor from different species			
A;Reference number: S33888; MUID:93261843			
A;Accession: S33888			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 68-92,97,'D',99-104 <GE2>			
A;Cross-references: EMBL:X99669			
C;Comment: This sequence contains five potential translation initiators: 1-Met, 28-Met, d is initiated from 1-Met.			
C;Superfamily: glucocorticoid receptor; erbA transforming protein homology <ERRBA>			
F;75-96/Region: DNA binding; nucleus; steroid hormone receptor; transcription regulation; z			
F;438-692/Domain: erbA transforming protein homology <ERRBA>			
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Job time: 836 sec

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